

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:01:59 ; Search time 32.09 Seconds  
(without alignments)  
303.844 Million cell updates/sec

**Title:** US-09-772-103-8  
**Perfect score:** 655  
**Sequence:** 1 MFQVQIFSFLLISAVILS.....CQWSSYPLTFGGGKVEIK 128  
**Scoring table:** BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```
Database :      PIR_68:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

## SUMMARIES

Result No.	Query No.	Score	% Match		Length	DB	ID	Description
			Match					
1	1	502	76.6		130	2	A32513	Ig kappa chain pre
2	2	499	76.2		130	1	JL0079	Ig kappa chain pre
3	3	498	76.0		235	2	S25058	Ig kappa chain pre
4	4	491	75.0		140	2	PL0013	Ig kappa chain pre
5	5	478	73.0		130	2	S04573	Ig kappa chain pre
6	6	466	71.1		130	2	B32456	Ig kappa chain pre
7	7	463.5	70.8		107	2	S36264	Ig lambda chain V
8	8	463.5	70.8		108	2	B49047	Ig kappa chain V r
9	9	463.5	70.8		125	2	S40349	Ig kappa chain V-J
10	10	455.5	69.5		129	2	S52793	Ig kappa chain V-J
11	11	454.5	69.4		107	2	S36269	Ig kappa chain V
12	12	454.5	69.4		129	2	S40317	Ig lambda chain V
13	13	454.5	69.4		129	2	S25789	Ig kappa chain - h
14	14	452.5	69.1		123	2	S40331	Ig kappa chain - h
15	15	452.5	69.1		125	2	S40333	Ig kappa chain V-J
16	16	451.5	68.9		108	2	S19674	Ig kappa chain V r
17	17	451.5	68.9		132	2	S40334	Ig kappa chain - h
18	18	447.5	68.3		125	2	S40316	Ig kappa chain - h
19	19	446	68.1		129	1	KVMS7B	Ig kappa chain pre
20	20	445.5	68.0		127	2	S40367	Ig kappa chain V-J
21	21	444.5	67.9		108	1	K1HURY	Ig kappa chain V-I
22	22	444.5	67.9		108	2	S36277	Ig lambda chain V
23	23	441.5	67.4		108	1	K1HUBN	Ig kappa chain V-I
24	24	441.5	67.4		117	2	S46371	Ig kappa chain V-J
25	25	441.5	67.4		125	2	S40350	Ig kappa chain - h
26	26	441	67.3		132	2	S05268	Ig kappa chain pre
27	27	439.5	67.1		129	2	S40369	Ig kappa chain - h
28	28	437.5	66.8		108	2	S36279	Ig lambda chain V
29	29	436.5	66.6		108	1	K1HURE	Ig kappa chain V-I

## ALIGNMENTS

RESULT 1  
A32513 Ig kappa chain precursor V region (MRL22) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C:Accession: A32513  
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duce  
J. Clin. Invest. 82, 852-860, 1988  
A:Title: Immunoglobulin kappa light chain variable region gene complex organ  
A:Reference number: A94689; MUID:88331394  
A:Accession: A32513  
A:Molecule type: DNA  
A:Residues: 1-130 <KOF>  
A:Cross-references: GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:g196944  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-113/Domain: Immunoglobulin homology <IMM>

anti-tetanus toxin  
anti-HIV envelope  
Ig kappa chain V-I-I  
Ig kappa chain V-J-J  
Ig kappa chain V-J-J  
Ig kappa chain V-I-I  
Ig kappa chain V-I-I  
Ig kappa chain - h  
Ig kappa chain pre  
Ig kappa chain V-J-J  
Ig kappa chain V r  
Ig kappa chain V-J-J  
Ig kappa chain - h  
Ig kappa chain v-i

A:Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation  
 R:Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.  
 Eur. J. Immunol. 22, 1627-1634, 1992  
 A:Title: Non-random features of the repertoire expressed by the members of one V kappa g  
 A:Reference number: A49044; MUID:92289826  
 A:Accession: A49044  
 A:Molecule type: DNA  
 A:Residues: 1-25 <ML>  
 A:Cross-references: GB:S37663; NID:g250214; PIDN:AA22331.1; PID:g250217  
 A:Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)  
 A:Accession: B49044  
 A:Molecule type: DNA  
 A:Residues: 114-116 <ML>  
 A:Cross-references: GB:S37664; NID:g250215; PIDN:AA22332.1; PID:g250218  
 A:Experimental source: BALB/c germ-line  
 A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit  
 A:Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)  
 C:Genetics:  
 A:Gene: V(kappa)Ox1  
 A:Introns: 17/1  
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 A:Disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-130/Product: Ig kappa chain V region (6f6) #status predicted <MAT>  
 F:38-111/Domain: immunoglobulin homology <IMM>  
 F:45-109/Disulfide bonds: #status predicted

Query Match 76.2%; Score 499; DB 1; Length 130;  
 Best Local Similarity 74.2%; Pred. No. 3.3e-33;  
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISAVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITMSWYQOK 60  
 DB 1 MDFQVQIFSFLLISAVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITMSWYQOK 60  
 QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDTLTLSLQPEDFATYYCQWSSYPLTFG 120  
 DB 61 SGTSPKRWIYDTSNLASGVPSRFGSGSGTDTLTLSLQPEDFATYYCQWSSYPLTFG 120  
 QY 121 GGTKEIK 128  
 DB 121 AGTKLEK 128  
 RESULT 3  
 S04573  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000  
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
 A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific m  
 A:Reference number: S25057  
 A:Accession: S25058  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <FIS>  
 A:Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 498; DB 2; Length 235;  
 Best Local Similarity 74.2%; Pred. No. 7e-33;  
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISAVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITMSWYQOK 60  
 DB 1 MDFQVQIFSFLLISAVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITMSWYQOK 60

QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDTLTLSLQPEDFATYYCQWSSYPLTFG 120  
 DB 61 SGTSPKRWIYDTSNLASGVPSRFGSGSGTDTLTLSLQPEDFATYYCQWSSYPLTFG 120  
 QY 121 GGTKEIK 128  
 DB 121 AGTKLEK 128  
 RESULT 4  
 S04573  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
 C:Accession: PL0013  
 R:Cheng, H.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.  
 Mol. Immunol. 25, 33-40, 1988  
 A:Title: Structural basis of stimulatory anti-idiotypic antibodies.  
 A:Reference number: PL0011; MUID:88142863  
 A:Accession: PL0013  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <CHE>  
 A:Experimental source: cell line 4C11  
 C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>  
 F:38-111/Domain: immunoglobulin homology <IMM>  
 F:46-55/Region: complementarity-determining 1  
 F:71-77/Region: complementarity-determining 2  
 F:110-118/Region: complementarity-determining 3  
 F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 75.0%; Score 491; DB 2; Length 140;  
 Best Local Similarity 74.2%; Pred. No. 1.5e-32;  
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISAVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITMSWYQOK 60  
 DB 1 MHFQVQIFSFLLISAVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITMSWYQOK 60  
 QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDTLTLSLQPEDFATYYCQWSSYPLTFG 120  
 DB 61 PDTSPKRWIYDTSNLASGVPSRFGSGSGTDTLTLSLQPEDFATYYCQWSSYPLTFG 120  
 QY 121 GGTKEIK 128  
 DB 121 GGTKEIK 128  
 RESULT 5  
 S04573  
 C:Species: Mus musculus (house mouse)  
 C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000  
 C:Accession: S04573  
 R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;  
 Eur. J. Immunol. 17, 91-95, 1987  
 A:Title: Molecular analysis of the murine lupus-associated anti-self response: invol  
 A:Reference number: S04573; MUID:87133856  
 A:Accession: S04573  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <KOF>  
 A:Cross-references: EMBL:X14620; NID:g52031; PIDN:CAA32773.1; PID:g52032  
 A:Note: the authors translated the codon AGC for residue 47 as Asn  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>  
 F:38-113/Domain: immunoglobulin homology <IMM>



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Qy      82  RFGSGSGTDYTLTISSLPQDFATYYCQWSSYPLTFGGGTKVEIK 120
      |||
Db      61  RFGSGSGTDFTLTISSLPQDFATYYCQTTSPFLTFGGGTKLEIK 107
      |||

RESULT  12
S40317
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 sequence_revision 26-May-1995 #text_chain
C:Accession: S40317
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their h
A:Reference number: S40312; MUID:94080891
A:Accession: S40317
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72427; NID:g441322; PIDN:CAA51095.1
C:Superfamily: immunoglobulin V region; immunoglobulin homolo
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match      69.4%; Score 454.5; DB 2; Length:
Best Local Similarity 81.8%; Pred. No. 1.1e-29;
Matches 90; Conservative 7; Mismatches 12; Indels:

Qy      20  SRGDIQMTQSPSSLSASVGRVITTCATSSI-IYMSHYQKPKGKAPKLIT
      :|
Db      19  ARCDIQMTQSPSLSTSLGDRVITTCRASQSIGTYLNWYQKPKGKAPKFL
      :|

Qy      79  VPSRFSGSGSDTYTITISLPQDFATYYCQWSSYPLTFGGGTKVEIK
      :|
Db      79  VPSRFSGSGSDTYTITISLPQDFATYYCQTTSTPTTFGGGTKVEIK
      :|

RESULT  13
S52789
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_chain
C:Accession: S52789
R:Rocca, A.; Khamlichchi, A.A.; Touchard, G.; Mougnot, B.; Rou
submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction a
A:Reference number: S52789
A:Accession: S52789
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.
C:Superfamily: immunoglobulin V region; immunoglobulin homolo
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match      69.4%; Score 454.5; DB 2; Length:
Best Local Similarity 71.0%; Pred. No. 1.1e-29;
Matches 93; Conservative 15; Mismatches 18; Indels:

Qy      1  MDPQV-QIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCAT
      |||
Db      1  MDMPVPAQLGLGLLWLSSG--ARCDIQMTQSPSSLSASVGRVITTCQAS
      |||

Qy      58  QOKPKAPKLLIYDTSNLASGVPSRFSGSGSDTYTITISLPQDFATY
      |||
Db      59  QOKPKAPKLLIHAASSLETGVPFRFSGSGSDTDFSTISSLPQDFATY
      |||

Qy      118  TFGGGTKVEIK 128
      |||

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[illegible]

